



7600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/903,806C

DATE: 10/07/2003

TIME: 09:35:23

RECEIVED

OCT 15 2003

Input Set : A:\P1618P2C3 sequence listing.txt

Output Set: N:\CRF4\10072003\I903806C.raw

TECH CENTER 1600/2900

7 <110> APPLICANT: Chen, Jian
 8 Goddard, Audrey
 9 Gurney, Austin L.
 10 Hillan, Kenneth
 11 Pennica, Diane
 12 Wood, William I.
 13 Yuan, Jean
 15 <120> TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 16 Acids Encoding the Same
 18 <130> FILE REFERENCE: P1618P2C3
 20 <140> CURRENT APPLICATION NUMBER: US 09/903,806C
 21 <141> CURRENT FILING DATE: 2001-07-11
 23 <150> PRIOR APPLICATION NUMBER: US 09/665,350
 24 <151> PRIOR FILING DATE: 2000-09-18
 26 <150> PRIOR APPLICATION NUMBER: PCT/US00/04414
 27 <151> PRIOR FILING DATE: 2000-02-22
 29 <150> PRIOR APPLICATION NUMBER: PCT/US98/18824
 30 <151> PRIOR FILING DATE: 1998-09-10
 32 <150> PRIOR APPLICATION NUMBER: US 60/062,287
 33 <151> PRIOR FILING DATE: 1997-10-17
 35 <160> NUMBER OF SEQ ID NOS: 424
 37 <210> SEQ ID NO: 1
 38 <211> LENGTH: 1825
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Homo Sapien
 42 <400> SEQUENCE: 1
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 45 cctcgacctc gacccacgcg tccgggccgg agcagcacgg ccgcaggacc 100
 47 tggagctccg gctgcgtctt cccgcagcgc taccgcctat gcgcctgccg 150
 49 cgccggggccg cgctggggct cctgccgctt ctgctgctgc tgccgcccgc 200
 51 gccggaggcc gccaaagaagc cgacgccctg ccaccgggtg cggggggctgg 250
 53 tggacaagtt taaccagggg atggtggaca ccgcaaagaa gaactttggc 300
 55 ggcgggaaca cggcttgga ggaaaagacg ctgtccaagt acgagtccag 350
 57 cgagattcgc ctgctggaga tcctggaggg gctgtgagag agcagcgact 400
 59 tcgaatgcaa tcagatgcta gaggcgcagg aggagcacct ggaggcctgg 450
 61 tggctgcagc tgaagagcga atatactgac ttattcgagt ggttttgtgt 500
 63 gaagacactg aaagtgtgct gctctccagg aacctacggt cccgactgtc 550
 65 tcgcatgccg gggcggtacc cagaggccct gcagcgggaa tggccactgc 600
 67 agcggagatg ggagcagaca gggcgacggg tcctgccggt gccacatggg 650
 69 gtaccagggc ccgctgtgca ctgactgcat ggacggctac ttcagctcgc 700
 71 tccggaacga gacccacagc atctgcacag cctgtgacga gtcctgcaag 750
 73 acgtgctcgg gcctgaccaa cagagactgc ggcgagtgtg aagtgggctg 800
 75 ggtgctggac gagggcgccct gtgtggatgt ggacgagtgt gcggccgagc 850

ENTERED

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77 . cgctccctg cagcgctgcg cagttctgta agaacgccaa cggctcctac 900
79 acgtgcgaag agtgtgactc cagctgtgtg ggctgcacag gggaaggccc 950
81 aggaaactgt aaagagtgtg tctctggcta cgcgaggag cacggacagt 1000
83 gtgcagatgt ggacgagtgc tctactagcag aaaaaacctg tgtgaggaaa 1050
85 aacgaaaact gctacaatac tccaggagagc tacgtctgtg tgtgtcctga 1100
87 cggcttcgaa gaaacggaag atgcctgtgt gccgccggca gaggctgaag 1150
89 ccacagaagg agaaagcccg acacagctgc cctcccgcga agacctgtaa 1200
91 tgtgccggac ttacccttta aattattcag aaggatgtcc cgtggaaaat 1250
93 gtggccctga ggatgccgtc tcctgcagtg gacagcggcg gggagaggct 1300
95 gcctgctctc taacggttga ttctcatttg tcccttaaac agctgcattt 1350
97 cttggttgtt cttaaacaga cttgtatatt ttgatacagt tctttgtaat 1400
99 aaaattgacc attgtaggta atcaggagga aaaaaaaaaa aaaaaaaaaa 1450
101 aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgccatg 1500
103 gcccaacttg tttattgcag cttataatgg ttacaaataa agcaatagca 1550
105 tcacaaattht cacaaataaa gcattttttt cactgcattc tagttgtggt 1600
107 ttgtccaaac tcatcaatgt atcttatcat gtctggatcg ggaattaatt 1650
109 cggcgcagca ccatggcctg aaataacctc tgaaagagga acttggttag 1700
111 gtaccttctg aggcggaag aaccagctgt ggaatgtgtg tcagttaggg 1750
113 tgtggaaagt cccagggctc cccagcaggc agaagtatgc aagcatgcat 1800
115 ctcaattagt cagcaacca gtttt 1825

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117 <210> SEQ ID NO: 2

118 <211> LENGTH: 353

119 <212> TYPE: PRT

120 <213> ORGANISM: Homo Sapien

122 <400> SEQUENCE: 2

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123 Met Arg Leu Pro Arg Arg Ala Ala Leu Gly Leu Leu Pro Leu Leu
124   1           5           10           15
126 Leu Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro
127           20           25           30
129 Cys His Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met
130           35           40           45
132 Val Asp Thr Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp
133           50           55           60
135 Glu Glu Lys Thr Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu
136           65           70           75
138 Leu Glu Ile Leu Glu Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys
139           80           85           90
141 Asn Gln Met Leu Glu Ala Gln Glu Glu His Leu Glu Ala Trp Trp
142           95          100          105
144 Leu Gln Leu Lys Ser Glu Tyr Pro Asp Leu Phe Glu Trp Phe Cys
145          110          115          120
147 Val Lys Thr Leu Lys Val Cys Cys Ser Pro Gly Thr Tyr Gly Pro
148          125          130          135
150 Asp Cys Leu Ala Cys Gln Gly Gly Ser Gln Arg Pro Cys Ser Gly
151          140          145          150
153 Asn Gly His Cys Ser Gly Asp Gly Ser Arg Gln Gly Asp Gly Ser
154          155          160          165
156 Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu Cys Thr Asp Cys
157          170          175          180

```

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159 Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr His Ser Ile
160                               185                               190                               195
162 Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly Leu Thr
163                               200                               205                               210
165 Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp Glu
166                               215                               220                               225
168 Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro
169                               230                               235                               240
171 Cys Ser Ala Ala Gln Phe Cys Lys Asn Ala Asn Gly Ser Tyr Thr
172                               245                               250                               255
174 Cys Glu Glu Cys Asp Ser Ser Cys Val Gly Cys Thr Gly Glu Gly
175                               260                               265                               270
177 Pro Gly Asn Cys Lys Glu Cys Ile Ser Gly Tyr Ala Arg Glu His
178                               275                               280                               285
180 Gly Gln Cys Ala Asp Val Asp Glu Cys Ser Leu Ala Glu Lys Thr
181                               290                               295                               300
183 Cys Val Arg Lys Asn Glu Asn Cys Tyr Asn Thr Pro Gly Ser Tyr
184                               305                               310                               315
186 Val Cys Val Cys Pro Asp Gly Phe Glu Glu Thr Glu Asp Ala Cys
187                               320                               325                               330
189 Val Pro Pro Ala Glu Ala Glu Ala Thr Glu Gly Glu Ser Pro Thr
190                               335                               340                               345
192 Gln Leu Pro Ser Arg Glu Asp Leu
193                               350
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196 <211> LENGTH: 2206
197 <212> TYPE: DNA
198 <213> ORGANISM: Homo Sapien
200 <400> SEQUENCE: 3
201 caggtccaac tgcacctcgg ttctatcgat tgaattcccc ggggatacctc 50
203 tagagatccc tcgacctcga cccacgcgtc cgccaggccg ggaggcgacg 100
205 cgcccagccg tctaaacggg aacagccctg gctgaggagag ctgcagcgca 150
207 gcagagtatc tgacggcgcc aggttgcgta ggtgcggcac gaggagtttt 200
209 cccggcagcg aggaggtcct gagcagcatg gcccgaggga gcgccttccc 250
211 tgccgccgcg ctctggctct ggagcactct cctgtgcctg ctggcactgc 300
213 gggcggaggc cgggccgccg caggaggaga gcctgtacct atggatcgat 350
215 gctcaccagg caagagtact cataggattt gaagaagata tcctgattgt 400
217 ttcagagggg aaaatggcac cttttacaca tgatttcaga aaagcgcaac 450
219 agagaatgcc agctattcct gtcaatatcc attccatgaa ttttacctgg 500
221 caagctgcag ggcaggcaga atacttctat gaattcctgt ccttgcgctc 550
223 cctggataaa ggcacatcgg cagatccaac cgtcaatgtc cctctgctgg 600
225 gaacagtgcc tcacaaggca tcagttgttc aagttggttt cccatgtcct 650
227 ggaaaacagg atgggggtggc agcatttgaa gtggatgtga ttgttatgaa 700
229 ttctgaaggc aacaccattc tccaaacacc tcaaaatgct atcttcttta 750
231 aaacatgtca acaagctgag tgcccaggcg ggtgccgaaa tggaggcttt 800
233 tgtaatgaaa gacgcactct cgagtgtcct gatgggttcc acggacctca 850
235 ctgtgagaaa gccctttgta cccacgatg tatgaatggg ggactttgtg 900
237 tgactcctgg tttctgcatc tgcccacctg gattctatgg agtgaactgt 950
239 gacaaagcaa actgctcaac cacctgcttt aatggaggga cctgtttcta 1000

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241 ccctggaaaa tgtatttgcc ctccaggact agagggagag cagtgtgaaa 1050
243 tcagcaaatg cccacaaccc tgtcgaaatg gaggtaaatg cattggtaaa 1100
245 agcaaatgta agtgttccaa aggttaccag ggagacctct gttcaaagcc 1150
247 tgtctgcgag cctggctgtg gtgcacatgg aacctgccat gaacccaaca 1200
249 aatgccaatg tcaagaaggt tggcatggaa gacactgcaa taaaaggtac 1250
251 gaagccagcc tcatacatgc cctgaggcca gcaggcgccc agctcaggca 1300
253 gcacacgcct tcacttaaaa aggccgagga gcggcgggat ccacctgaat 1350
255 ccaattacat ctggtgaact ccgacatctg aaacgtttta agttacacca 1400
257 agttcatagc ctttggttaac ctttcatgtg ttgaatgttc aaataatgtt 1450
259 cattacactt aagaatactg gcctgaattt tattagcttc attataaatc 1500
261 actgagctga tatttactct tccttttaag ttttctaagt acgtctgtag 1550
263 catgatggta tagattttct tgtttcagtg ctttgggaca gattttatat 1600
265 tatgtcaatt gatcagggtta aaattttcag tgtgtagttg gcagatattt 1650
267 tcaaaattac aatgcattta tgggtgtctgg gggcagggga acatcagaaa 1700
269 gggttaaattg ggcaaaaatg cgtaagtcac aagaatttgg atggtgcagt 1750
271 taatgttgaa gttacagcat ttcagatttt attgtcagat atttagatgt 1800
273 ttgttacatt tttaaaaatt gctcttaatt tttaaactct caatacaata 1850
275 tattttgacc ttaccattat tccagagatt cagtattaaa aaaaaaaaaa 1900
277 ttacactgtg gtagtggcat ttaaacaata taatatattc taaacacaat 1950
279 gaaataggga atataatgta tgaacttttt gcattggctt gaagcaatat 2000
281 aatatattgt aaacaaaaca cagctcttac ctaataaaca ttttatactg 2050
283 tttgtatgta taaaataaag gtgctgcttt agtttttttg aaaaaaaaaa 2100
285 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggcgccgc gactctagag 2150
287 tcgacctgca gaagcttggc cgccatggcc caacttgttt attgcagctt 2200
289 ataattg 2206

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291 <210> SEQ ID NO: 4

292 <211> LENGTH: 379

293 <212> TYPE: PRT

294 <213> ORGANISM: Homo Sapien

296 <400> SEQUENCE: 4

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297 Met Ala Arg Arg Ser Ala Phe Pro Ala Ala Ala Leu Trp Leu Trp
298   1           5           10           15
300 Ser Ile Leu Leu Cys Leu Leu Ala Leu Arg Ala Glu Ala Gly Pro
301           20           25           30
303 Pro Gln Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala
304           35           40           45
306 Arg Val Leu Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu
307           50           55           60
309 Gly Lys Met Ala Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln
310           65           70           75
312 Arg Met Pro Ala Ile Pro Val Asn Ile His Ser Met Asn Phe Thr
313           80           85           90
315 Trp Gln Ala Ala Gly Gln Ala Glu Tyr Phe Tyr Glu Phe Leu Ser
316           95          100          105
318 Leu Arg Ser Leu Asp Lys Gly Ile Met Ala Asp Pro Thr Val Asn
319          110          115          120
321 Val Pro Leu Leu Gly Thr Val Pro His Lys Ala Ser Val Val Gln
322          125          130          135
324 Val Gly Phe Pro Cys Leu Gly Lys Gln Asp Gly Val Ala Ala Phe

```

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325          140          145          150
327  Glu Val Asp Val Ile Val Met Asn Ser Glu Gly Asn Thr Ile Leu
328          155          160          165
330  Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr Cys Gln Gln Ala
331          170          175          180
333  Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Glu Arg
334          185          190          195
336  Arg Ile Cys Glu Cys Pro Asp Gly Phe His Gly Pro His Cys Glu
337          200          205          210
339  Lys Ala Leu Cys Thr Pro Arg Cys Met Asn Gly Gly Leu Cys Val
340          215          220          225
342  Thr Pro Gly Phe Cys Ile Cys Pro Pro Gly Phe Tyr Gly Val Asn
343          230          235          240
345  Cys Asp Lys Ala Asn Cys Ser Thr Thr Cys Phe Asn Gly Gly Thr
346          245          250          255
348  Cys Phe Tyr Pro Gly Lys Cys Ile Cys Pro Pro Gly Leu Glu Gly
349          260          265          270
351  Glu Gln Cys Glu Ile Ser Lys Cys Pro Gln Pro Cys Arg Asn Gly
352          275          280          285
354  Gly Lys Cys Ile Gly Lys Ser Lys Cys Lys Cys Ser Lys Gly Tyr
355          290          295          300
357  Gln Gly Asp Leu Cys Ser Lys Pro Val Cys Glu Pro Gly Cys Gly
358          305          310          315
360  Ala His Gly Thr Cys His Glu Pro Asn Lys Cys Gln Cys Gln Glu
361          320          325          330
363  Gly Trp His Gly Arg His Cys Asn Lys Arg Tyr Glu Ala Ser Leu
364          335          340          345
366  Ile His Ala Leu Arg Pro Ala Gly Ala Gln Leu Arg Gln His Thr
367          350          355          360
369  Pro Ser Leu Lys Lys Ala Glu Glu Arg Arg Asp Pro Pro Glu Ser
370          365          370          375
372  Asn Tyr Ile Trp
375 <210> SEQ ID NO: 5
376 <211> LENGTH: 45
377 <212> TYPE: DNA
378 <213> ORGANISM: Artificial Sequence
380 <220> FEATURE:
381 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
383 <400> SEQUENCE: 5
384  agggagcacg gacagtgtgc agatgtggac gactgctcac tagca 45
386 <210> SEQ ID NO: 6
387 <211> LENGTH: 21
388 <212> TYPE: DNA
389 <213> ORGANISM: Artificial Sequence
391 <220> FEATURE:
392 <223> OTHER INFORMATION: Synthetic Oligonucleotide Probe
394 <400> SEQUENCE: 6
395  agagtgtatc tctggctacg c 21
397 <210> SEQ ID NO: 7

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/903,806C

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Input Set : A:\P1618P2C3 sequence listing.txt
Output Set: N:\CRF4\10072003\I903806C.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 33,37,80,94,144,188

Seq#:26; N Pos. 21

Seq#:50; N Pos. 61

Seq#:113; N Pos. 1461

Seq#:131; N Pos. 1837

Seq#:174; N Pos. 1683

Seq#:175; Xaa Pos. 539

Seq#:206; N Pos. 973,977,996,1003

Seq#:424; Xaa Pos. 1,3,4,5,6,7,8,9,11,12,13,14,15,17,18,19,20,21,22,23,24

Seq#:424; Xaa Pos. 25,26,28,30,31,32,33,34,36,37,39

VERIFICATION SUMMARY

DATE: 10/07/2003

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Input Set : A:\P1618P2C3 sequence listing.txt

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L:585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
M:341 Repeated in SeqNo=13
L:902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0
L:2087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50 after pos.:50
L:4499 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:113 after pos.:1450
L:5070 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:131 after pos.:1800
L:6720 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:174 after pos.:1650
L:6896 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:175 after pos.:525
L:8258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:206 after pos.:950
M:341 Repeated in SeqNo=206
L:15200 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:424 after pos.:0
M:341 Repeated in SeqNo=424